The cospeciation between massive corals and gall crabs.(Digest_要約)

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CITATION:

Zayasu, Yuna. The cospeciation between massive corals and gall crabs.. 京都大学, 2014, 博士(理学)

ISSUE DATE:

2014-03-24

URL:

https://doi.org/10.14989/doctor.k18105

The cospeciation between massive corals and gall crabs

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Abstract

Background

Coral reefs are known as one of the most biologically diverse ecosystem in the world, although the coral reefs cover less than 1.2 percent of the world's continental shelf area and only 0.09 percent of the total area of the world's oceans. These scarce areas caused by highly complex structure of a variety of corals, provide habitats and refuges for more than 1 million species of plants and animals. However, compared to studies on terrestrial biota, researches on marine species interaction remain scarce. The host specificity and host-parasite interactions can be thought to contribute to note only species richness, but also evolutionary diversifications of symbiotic.

Family Cryptochiridae Paul'son, 1875, is one of the dominant obligatory associate of massive corals as well as barnacles. The cryptochirid crabs known as gall crabs or pit crabs. They live within the skeleton of scleractinian corals by causing the growing coral to form various types of galls or pits around them. However, there have been no detailed investigations about their host specificity and the evolutionary relationships between their host corals.

Outline

To reveal the relationships between *Fizesereneia* Takeda and Tamura, 1980 (Crustacea: Decapoda: Brachyura: Cryptochiridae) and their host scleractinian corals, the specimens were collected. However, the classification problems of both taxa have not fully resolved. First, the phylogenetic relationships of coral family Lobophylliidae are reconstructed in chapter 1, and species boundaries of *Acanthastrea hemprichii* species complex are discussed in chapter 2. Subsequently, A systematic study for the Japanese species of pit crabs genus *Fizesereneia* is made in chapter 3. Finally, the molecular phylogenetic relationships between host Lobophylliidae corals and symbiotic *Fizesereneia* crabs are compared in chapter 4.

Chapter 1

The purposes of chapter 1, are to reconstruct phylogenetic relationships of family Lobophylliidae including taxonomic positions of some genera in these clades with partial mitochondrial DNA cytochrome c oxidase subunit 1 (mtDNA COI) sequences, and to discuss the validity of name of their taxon. I present data from 18 species of 51 species that currently recognized species in Lobophylliidae. The present study indicates *Echinomorpha nishihirai* is related to clade XIX-A which is the same clade as *Echinophyllia aspera* and *Oxypora lacera*. *Acanthastrea ishigakiensis* is closer to *Lobophyllia* and *Symphyllia* than the others congeneric species. *Echinophyllia echinata* is closer to *Pectinia lactuca, P. ayleni, P. alcicornis* and *Mycedium elephantotus* than the others congeneric species.

Chapter 2

To reveal species boundary between the members of the *Acanthastrea hemprichii* complex (*A. hemprichii, A. echinata, A. rotundoflora*), analyses were conducted for molecular level, based on a mitochondrial noncording region (1031 bp) between CO1 and lrRNA and the nuclear β-tubulin DNA fragments (1509 bp), as well as difference in geographical distribution, reproductive isolation, and macro-morphological analyses. (1) In *Acanthastrea hemprichii*, the three morphotypes have the high fertilization rate (average over 70%) in each combination, and no difference was observed on the spawning time among the members. Therefore, we have concluded that morphological differences seen in these three morphotypes are intraspecific variation. Moreover, a clade consisting of specimens collected only from temperate areas has been recognized, and its nucleotide diversity is much lower than those from other places. This result indicates that the bottleneck effect occurred for the temperate population. (2) In present study, the differences were observed in morphology and geographical distribution between *Acanthastrea hemprichii* and *Acanthastrea echinata*. (3) The phylogenetic evidence can be considered that *A. hemprichii* retained ancestral polymorphism based on the presence of a temperate specific clade. Therefore, when comparing the results of molecular analyses using a nuclear maker if this temperate specific clade is removed, significant genetic differences are detected among three species, *A. hemprichii, A. echinata* and *A. rotundoflora*.

Chapter 3

A systematic review of the Japanese species of the genus *Fizesereneia* Takeda and Tamura, 1980, from Japan is presented. Four species of six are rediagnosed, and the gill structures and mouthparts of them are described and illustrated for the first time.

Chapter 4

The extent of parallel cladogenesis in association between the obligate *Fizesereneia* crabs and their host corals were assessed by the reconstruction of the phylogenetic relationships and morphological analysis. To estimate the phylogeny, I used DNA sequences of mitochondrial cytochrome oxidase subunit I gene for four species of *Fizesereneia* crabs, and nuclear β-tubulin gene for host corals. The results of this study indicate significant high host specificity and the congruence phylogenies between *Fizesereneia* and host corals.